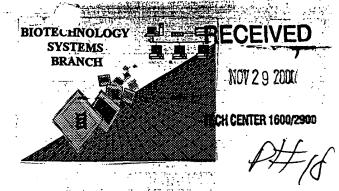# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/555,981_

Source: _1642_

Date Processed by STIC: _11/16/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	

SERIAL NUMBER: _09/555,981_

RECEIVED
APR 29 ...
TECH CENTER 1600/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES) — Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES) — Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

B.TeDeschi

RAW SEQUENCE LISTING   DATE: 11/16/2000
PATENT APPLICATION: US/09/555,981   TIME: 19:24:38

Input Set : A:\Leadd bl.app
Output Set: N:\CRF3\11162000\I555981.raw

```
 3 <110> APPLICANT: Noteborn, Mathieu Hubertus Maria
 4         Danen-Van Oorschot, Astrid Adriana Anna Maria
 6 <120> TITLE OF INVENTION: Molecules Ineracting with Apoptin
 8 <130> FILE REFERENCE: LEBV.006.01
10 <140> CURRENT APPLICATION NUMBER: 09/555,981
11 <141> CURRENT FILING DATE: 1998-12-03
13 <150> PRIOR APPLICATION NUMBER: PCT/NL98/00687
14 <151> PRIOR FILING DATE: 1998-12-03
16 <150> PRIOR APPLICATION NUMBER: 97203781.6 EP
17 <151> PRIOR FILING DATE: 1997-12-03
19 <160> NUMBER OF SEQ ID NOS: 13
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 658
25 <212> TYPE: DNA
26 <213> ORGANISM: Apoptin-Associating Clone
28 <400> SEQUENCE: 1
29 gggggatcat ggaagctgat aaagatgaca cacaacaaat tcttaaggag cattcgccag 60
30 atgaatttat aaaagatgaa caaaataagg gactaattga tgaaattaca aagaaaaata 120
31 ttcaactaaa gaaggagatc caaaagcttg aaacggagtt acaagaggct accaaagaat 180
32 tccagattaa agaggatatt cctgaaacaa agatgaaatt cttatcagtt gaaactcctg 240
33 agaatgacag ccagttgtca aatatctcct gttcgtttca agtgagctcg aaagttcctt 300
34 atgagataca aaaaggacaa gcacttatca cctttgaaaa agaagaagtt gctcaaaatg 360
35 tggtaagcat gagtaaacat catgtacaga taaaagatgt aaatctggag gttacggcca 420
36 agccagttcc attaaattca ggagtcagat tccaggttta tgtagaagtt tctaaaatga 480
37 aaatcaatgt tactgaaatt cctgacacat tgcgtgaaga tcaaatgaga gacaaactag 540
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W--> 38 agctgagctt ttcaaagtcc cgaaatggga ggcggagagg tggaccgcgt gggactatga 600
W--> 39 cagacagtcc gggagtgcag tcatcacgtt tggnggagat tgggagtggc tgacannn   658
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42 <210> SEQ ID NO: 2
43 <211> LENGTH: 717
44 <212> TYPE: DNA
45 <213> ORGANISM: Apoptin-Associating Clone
47 <400> SEQUENCE: 2
48 cggagttaca agaggctacc aaagaattcc agattaaaga ggatattcct gaaacaaaga 60
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W--> 49 tgaaattctt atcagttgaa actcctgana atgacagcca gttgtcaaat atctcctgtt 120
```
50 cgtttcaagg tgagctcgaa agttccttat gagatacaaa aaggacaatg cacttatcac 180
```
W--> 51 ctttgaaaaa ggaagaagtt gctcaaaatg tgngtaagca tgagtaaaca tcatgtacag 240
```
52 ataataagat gtaaatctgg aggttacggc caaagccaag ttccattaat attcaaggag 300
```
W--> 53 tcangattcc agngttatgc tagaangttt ctaaaaatga naatcaatgg ttactggaaa 360
W--> 54 ttcctggaca cattgcgntg aaagatcaag atgacgaaga caaactaaga agctgagctt 420
W--> 55 ttcaaaagtc ccgaaanatg gaagagcggt agagggtggn accgcgtgng anctatgaca 480
W--> 56 agacaagncc ggggaagntg cagtccatca cgtttgtnng aagattggan gtnggctgac 540
W--> 57 caangaattt tgaaaaagga gangaattac ccctctttan gagtaaantc aaaaccctgc 600
W--> 58 cataanaagt tnactggttt cncccattac acagnantta cannttganc aanantannc 660
W--> 59 aggataattt ncagggggaan aatctnaagn atggcaagnt gacttctgga caanggt   717
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62 <210> SEQ ID NO: 3
63 <211> LENGTH: 219
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RAW SEQUENCE LISTING   DATE: 11/16/2000
PATENT APPLICATION: US/09/555,981   TIME: 19:24:38

Input Set : A:\Leadd b1.app
Output Set: N:\CRF3\11162000\I555981.raw

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64 <212> TYPE: PRT
65 <213> ORGANISM: Apoptin-Associating Clone
67 <400> SEQUENCE: 3
68 His Glu Gly Arg Gly Ile Met Glu Ala Asp Lys Asp Asp Thr Gln Gln
69  1               5                   10                  15
71 Ile Leu Lys Glu His Ser Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn
72                  20                  25                  30
74 Lys Gly Leu Ile Asp Glu Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys
75              35                  40                  45
77 Glu Ile Gln Lys Leu Glu Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe
78      50                  55                  60
80 Gln Ile Lys Glu Asp Ile Pro Glu Thr Lys Met Lys Phe Leu Ser Val
81  65                  70                  75                  80
83 Glu Thr Pro Glu Asn Asp Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe
84                  85                  90                  95
86 Gln Val Ser Ser Lys Val Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu
87                  100                 105                 110
89 Ile Thr Phe Glu Lys Glu Glu Val Ala Gln Asn Val Val Ser Met Ser
90              115                 120                 125
92 Lys His His Val Gln Ile Lys Asp Val Asn Leu Glu Val Thr Ala Lys
93          130                 135                 140
95 Pro Val Pro Leu Asn Ser Gly Val Arg Phe Gln Val Tyr Val Glu Val
96 145                 150                 155                 160
98 Ser Lys Met Lys Ile Asn Val Thr Glu Ile Asp Asp Thr Leu Arg Glu
99              165                 170                 175
101 Asp Gln Met Arg Asp Lys Leu Glu Leu Ser Phe Ser Lys Ser Arg Asn
102              180                 185                 190
104 Gly Arg Arg Arg Cys Gly Pro Arg Gly Thr Met Thr Asp Ser Pro Gly
105          195                 200                 205
107 Val Gln Ser Ser Arg Leu Val Glu Ile Gly Ser
108     210                 215
111 <210> SEQ ID NO: 4
112 <211> LENGTH: 305
113 <212> TYPE: PRT
114 <213> ORGANISM: Apoptin-Associating Clone
116 <400> SEQUENCE: 4
117 Met Glu Ala Asp Lys Asp Asp Thr Gln Gln Ile Leu Lys Glu His Ser
118  1               5                   10                  15
120 Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn Lys Gly Leu Ile Asp Glu
121              20                  25                  30
123 Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys Glu Ile Gln Lys Leu Glu
124          35                  40                  45
126 Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe Gln Ile Lys Glu Asp Ile
127      50                  55                  60
129 Pro Glu Thr Lys Met Lys Phe Leu Ser Val Glu Thr Pro Glu Asn Asp
130  65                  70                  75                  80
132 Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe Gln Val Ser Ser Lys Val
133                  85                  90                  95
135 Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu Ile Thr Phe Glu Lys Glu
```

RAW SEQUENCE LISTING   DATE: 11/16/2000
PATENT APPLICATION: US/09/555,981   TIME: 19:24:38

Input Set : A:\Leadd bl.app
Output Set: N:\CRF3\11162000\I555981.raw

```
136              100              105              110
138 Glu Val Ala Gln Asn Val Val Ser Met Ser Lys His His Val Gln Ile
139              115              120              125
141 Lys Asp Val Asn Leu Glu Val Thr Ala Lys Pro Val Pro Leu Asn Ser
142     130              135              140
144 Gly Val Arg Phe Gln Val Tyr Glu Val Ser Lys Met Lys Ile Asn Val
145 145              150              155              160
147 Thr Glu Ile Pro Asp Thr Leu Arg Glu Asp Gln Met Arg Asp Lys Leu
148              165              170              175
150 Glu Leu Ser Phe Ser Lys Phe Arg Asn Gly Gly Gly Glu Val Asp Arg
151              180              185              190
153 Val Asp Tyr Asp Arg Gln Ser Gly Ser Ala Val Ile Thr Phe Val Glu
154     195              200              205
156 Ile Gly Val Asp Lys Ile Leu Lys Lys Lys Glu Tyr Pro Leu Pro Ile
157     210              215              220
159 Asn Gln Thr Cys His Arg Val Thr Val Ser Pro Tyr Thr Glu Ile His
160 225              230              235              240
162 Leu Lys Lys Tyr Gln Ile Phe Ser Gly Thr Ser Lys Arg Thr Val Leu
163              245              250              255
165 Leu Thr Gly Met Glu Gly Ile Gln Met Asp Glu Glu Ile Val Glu Asp
166     260              265              270
168 Leu Ile Asn Ile His Phe Gln Arg Ala Lys Asn Gly Gly Gly Glu Val
169     275              280              285
171 Asp Val Val Lys Cys Ser Leu Gly Gln Pro His Ile Ala Tyr Phe Glu
172     290              295              300
174 Glu
175 305
178 <210> SEQ ID NO: 5
179 <211> LENGTH: 659
180 <212> TYPE: DNA
181 <213> ORGANISM: Apoptin-Associating Clone
183 <400> SEQUENCE: 5
184 agcaggtgct gcaacaaaag gagcacacga tcaacatgga ggagtgccgg ctgcgggtgc 60
185 aggtccagcc cttggagctg cccatggtca ccaccatcca ggtgtccagc cagttgagtg 120
186 gccggagggt gttggtcact ggatttcctg ccagcctcag gctgagtgag gaggagctgc 180
```
W--> 187 tggacaanct anagatcttc tttggcaaga ctaggaacgg aggtggcnat gtggacnttc 240
W--> 188 gggganctact gccagggant gtcatgctgg ggtttgctag ggatggagtg gctcancgtc 300
W--> 189 tgtgccaaat cggccatttc acagtgccac tgggtgggca gcangtccct ctgagagtct 360
W--> 190 ctccgtatgt gaatggggan atccagangg ctganatcag gtcncagcca nttccccgct 420
```
191 cggtactggt gctcaacatt cctgatatct tggatggccc ggagctgcat gacgtcctgg 480
```
W--> 192 anatccactt ccagaanccc acccgcgggg gcggagatgt aagacgccct gacagtcgta 540
W--> 193 ccccaaggac aacagggcct aacagtcttc acctcctgaa tcaaggctan gggcctcccc 600
W--> 194 cttctcatcc tccccacccc ccccgccaaa ggttctcaan actgggcctg ggctttntg 659
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197 <210> SEQ ID NO: 6
198 <211> LENGTH: 631
199 <212> TYPE: DNA
200 <213> ORGANISM: Apoptin-Associating Clone
202 <400> SEQUENCE: 6
203 ccaaagtggc tgagcaggtg ctgcaacaaa aggagcacac gatcaacatg gaggagtgcc 60
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Item 10

RAW SEQUENCE LISTING   DATE: 11/16/2000
PATENT APPLICATION: US/09/555,981   TIME: 19:24:38

Input Set : A:\Leadd b1.app
Output Set: N:\CRF3\11162000\I555981.raw

```
      204 ggctgcgggt gcaggtccag cccttggagc tgcccatggt caccaccatc caggtgtcca 120
      205 gccagttgag tggccggagg gtgttggtca ctggatttcc tgccagcctc aggctgagtg 180
      206 aggaggagct gctggacaag ctagagatct tctttggcaa gactaggaac ggaggtggcg 240
      207 atgtggacgt tcgggagcta ctgccaggga gtgtcatgct ggggtttgct aggqatggag 300
W--> 208 tggctcagcg tctgtgccaa atcggccaag ttcacagtgc cactgggtgg gcancaagtc 360
W--> 209 cctctgagag tctctccgta tgtgaatggg gagatccaga aggctgagat caggtcgcan 420
W--> 210 ccagttcccc nctcggtact gggtgctcaa cattcctgat atcttggatt ggcccggagc 480
W--> 211 tgcatnacgt cctgganatc aacttcanaa gcccacccgc cggggcngng aggtanaagg 540
W--> 212 cctgacatcn ttaccccaaa ggacagcatg gncctaacag tcctcacctc cnaatcangc 600
W--> 213 tnngggggctn cccttctanc ntccccaact g                                631
      216 <210> SEQ ID NO: 7
      217 <211> LENGTH: 629
      218 <212> TYPE: DNA
      219 <213> ORGANISM: Apoptin-Associating Clone
      221 <400> SEQUENCE: 7
      222 ggatccactg ccctctgctt gcgggctctg ctctgatcac ctttgatgac cccaaagtgg 60
      223 ctgagcaggt gctgcaacaa aaggagcaca cgatcaacat ggaggagtgc cggctgcggg 120
      224 tgcaggtcca gcccttggag ctgcccatgg tcaccaccat ccaggtgatg gtgtccaagc 180
W--> 225 canttgagtg gccggagggt gttggtcact ggatttcctg ccagcctcag gctgantgag 240
W--> 226 gaggagctgc tggacagcta tgagatcttc tttggcaana ctangaacg angtggcgat 300
      227 gtggacgttc gggagctact gccaggaagt gtcatgctgg ggtttgctac ggatggagtg 360
      228 gctcagcgtc tgtgccaaat cggccagttc acaagtgcca ctgggtgggc agcaagtccc 420
W--> 229 tctgagagtc tctccgtatg tgantggnga gatcagaatg ctganattaa gtcgcatcca 480
W--> 230 attcctcgct cnggtactgg tgctcannat cctganatct tggattggcc ccngantnca 540
W--> 231 tganatctgg nagattcaat tncanaagtc canccnncng ncgggaagta nangcccgan 600
W--> 232 anttcntnnc ntanggncag canngcctg                                    629
      235 <210> SEQ ID NO: 8
      236 <211> LENGTH: 138
      237 <212> TYPE: PRT
      238 <213> ORGANISM: Apoptin-Associating Clone
      240 <400> SEQUENCE: 8
      241 His Glu Gly Pro Lys Val Ala Glu Gln Val Leu Gln Gln Lys Glu His
      242  1               5                  10                  15
      244 Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln Val Gln Pro Leu
      245              20                  25                  30
      247 Glu Leu Pro Met Val Thr Thr Ile Gln Val Ser Ser Gln Leu Ser Gly
      248          35                  40                  45
      250 Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg Leu Ser Glu
      251      50                  55                  60
      253 Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly Lys Thr Arg Asn
      254 65                  70                  75                  80
      256 Gly Gly Gly Asp Val Asp Val Arg Glu Leu Leu Pro Gly Ser Val Met
      257              85                  90                  95
      259 Leu Gly Phe Ala Arg Asp Gly Val Ala Gln Arg Leu Cys Gln Ile Gly
      260             100                 105                 110
      262 Gln Val His Ser Ala Thr Gly Trp Ala Ser Ser Pro Ser Glu Ser Leu
      263             115                 120                 125
      265 Ser Val Cys Glu Trp Gly Asp Pro Glu Gly
      266         130                 135
```

```
                RAW SEQUENCE LISTING                    DATE: 11/16/2000
                PATENT APPLICATION:  US/09/555,981      TIME: 19:24:38

                Input Set : A:\Leadd b1.app
                Output Set: N:\CRF3\11162000\I555981.raw

269 <210> SEQ ID NO: 9
270 <211> LENGTH: 282
271 <212> TYPE: PRT
272 <213> ORGANISM: Apoptin-Associating Clone
274 <400> SEQUENCE: 9
275 Met Ser Ala Pro Leu Asp Ala Ala Leu His Ala Leu Gln Glu Glu Gln
276  1               5                  10                  15
278 Ala Arg Leu Lys Met Arg Leu Trp Asp Leu Gln Gln Leu Arg Lys Glu
279             20                  25                  30
281 Leu Gly Asp Ser Pro Lys Asp Lys Val Pro Phe Ser Val Pro Lys Ile
282         35                  40                  45
284 Pro Leu Val Phe Arg Gly His Thr Gln Gln Asp Pro Glu Val Pro Lys
285         50                  55                  60
287 Ser Leu Val Ser Asn Leu Arg Ile His Cys Pro Leu Leu Ala Gly Ser
288  65                  70                  75                  80
290 Ala Leu Ile Thr Phe Asp Asp Pro Lys Val Ala Glu Gln Val Leu Gln
291             85                  90                  95
293 Gln Lys Glu His Thr Ile Asn Met Glu Glu Cys Arg Leu Arg Val Gln
294             100                 105                 110
296 Val Gln Pro Leu Glu Leu Pro Met Val Thr Thr Ile Gln Val Ser Ser
297         115                 120                 125
299 Gln Leu Ser Gly Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu
300         130                 135                 140
302 Arg Leu Ser Glu Glu Glu Leu Leu Asp Lys Leu Glu Ile Phe Phe Gly
303 145                 150                 155                 160
305 Lys Thr Arg Asn Gly Gly Gly Asp Val Asp Val Arg Glu Leu Leu Pro
306             165                 170                 175
308 Gly Ser Val Met Leu Gly Phe Ala Arg Asp Gly Val Ala Gln Arg Leu
309             180                 185                 190
311 Cys Gln Ile Gly Gln Phe Thr Val Pro Leu Gly Gly Gln Gln Val Pro
312         195                 200                 205
314 Leu Arg Val Ser Pro Tyr Val Asn Gly Glu Ile Gln Lys Ala Glu Ile
315         210                 215                 220
317 Arg Ser Gln Pro Val Pro Arg Ser Val Leu Val Leu Asn Ile Pro Asp
318 225                 230                 235                 240
320 Ile Leu Asp Gly Pro Glu Leu His Asp Val Leu Glu Ile His Phe Gln
321             245                 250                 255
323 Lys Pro Thr Arg Gly Gly Gly Gly Arg Gly Pro Asp Ser Arg Thr Pro
324             260                 265                 270
326 Arg Thr Ala Gly Pro Ser Ser Leu His Leu
327         275                 280
330 <210> SEQ ID NO: 10
331 <211> LENGTH: 207
332 <212> TYPE: PRT
333 <213> ORGANISM: Apoptin-Associating Clone
335 <400> SEQUENCE: 10
336 His Glu Gly Arg Ile His Cys Pro Leu Leu Ala Gly Ser Ala Leu Ile
337  1               5                  10                  15
339 Thr Phe Asp Asp Pro Lys Val Ala Glu Gln Val Leu Gln Gln Lys Glu
```

FYI:

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 11/16/2000
PATENT APPLICATION: US/09/555,981   TIME: 19:24:40

Input Set : A:\Leadd bl.app
Output Set: N:\CRF3\11162000\I555981.raw

```
L:38 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:38 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:49 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:49 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:49 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:49 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:49 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:51 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:53 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:53 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:53 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:53 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:54 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
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L:55 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:55 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:55 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:56 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:57 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:58 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:59 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
```

VERIFICATION SUMMARY   DATE: 11/16/2000
PATENT APPLICATION: US/09/555,981   TIME: 19:24:40

Input Set : **A:\Leadd bl.app**
Output Set: **N:\CRF3\11162000\I555981.raw**

```
L:187 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:187 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:187 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:187 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:187 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:188 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:188 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:208 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:225 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:345 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:585 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
```